

gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca	1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala	
310 315 320	
agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac	1245
Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn	
325 330 335	
aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc	1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe	
340 345 350	
tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag	1341
Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu	
355 360 365 370	
aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac	1389
Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr	
375 380 385	
gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc	1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys	
390 395 400	
atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc	1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro	
405 410 415	
agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc	1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr	
420 425 430	
agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga	1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg	
435 440 445 450	
cag aag agt cca gcc tca tagtgccga gccatccctg tccccgtcag	1629
Gln Lys Ser Pro Ala Ser	
455	
cagtgtctgt gtgtctgcat aaaccctcct gtccctggacg tgacttcac ctaggagcc	1689
acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg	1749
tgctgccctg gcatcagcct cttccagtca catctggcca gagggctgtc tggacctggg	1809
ccctgctcaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac	1869
aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catcccatg ccccgctccg	1929
ggggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca	1989
gtttcctccc cagggcagag ctccccctcc tgcaagagtc tgggaggcgg tgcaggctgt	2049
cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg	2109
cggcaccact gggaactctg gacttgagtg tgtttctct tccttgggta tgaatgtgtg	2169

agttcaccca gaggcctgct ctcctcacac attgtgtggt ttgggggttaa tgatggaggg 2229
 agacacctct tcatagacgg caggtgcccc cctttcaggg agtctcccag catgggcgga 2289
 tgccggggcat gagctgctgt aaactatttg tggctgtgct gcttgagtga cgtctctgtc 2349
 gtgtgggtgc caagtgcttg tgtagaaact gtgttctgag ccccttttc tggacaccaa 2409
 ctgtgtcctg tgaatgtatc gctactgtga gctgttcccg cctagccagg gccatgtctt 2469
 aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctcggtgtct 2529
 cgggccacca tccgcccacc tcgggctgac cccacctcct ccatggacag tgtgagcccc 2589
 gggccgtgca tcctgctcag tgtggcgta gtgtcggggc tgagccccctt gagctgtctc 2649
 agtgaatgta cagtgcggcg cagcagctga acctcatgtg ttccactccc aataaaaggt 2709
 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2762

<210> 2
 <211> 456
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
 1 5 10 15
 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
 20 25 30
 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
 35 40 45
 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
 50 55 60
 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
 65 70 75 80
 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
 85 90 95
 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
 100 105 110
 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
 115 120 125
 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
 130 135 140
 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
 145 150 155 160

Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
165 170 175

Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
180 185 190

Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
195 200 205

Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
210 215 220

Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
225 230 235 240

Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
245 250 255

Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
260 265 270

Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
275 280 285

Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
290 295 300

Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
305 310 315 320

Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
325 330 335

Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
340 345 350

Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
355 360 365

Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
370 375 380

Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
385 390 395 400

Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
405 410 415

Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
420 425 430

Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
435 440 445

Asn Arg Gln Lys Ser Pro Ala Ser
450 455

[illegible][illegible][illegible]

ttt Phe	agg Arg	ggt Gly	gct Ala	caa Gln 175	atc Ile	att Ile	tct Ser	ggg Gly	caa Gln 180	gaa Glu	gaa Glu	ggg Gly	gta Val	tat Tyr	gga Gly 185	640
tgg Trp	att Ile	aca Thr	gcc Ala 190	aac Asn	tat Tyr	tta Leu	atg Met	gga Gly 195	aat Asn	ttc Phe	ctg Leu	gag Glu	aag Lys	aac Asn	ctg Leu	688
tgg Trp	cac His	atg Met 205	tgg Trp	gtg Val	cac His	ccg Pro	cat His 210	gga Gly	gtg Val	gaa Glu	acc Thr	acg Thr	ggg Gly	gcc Ala	ctg Leu	736
gac Asp	tta Leu 220	ggt Gly	ggt Gly	gcc Ala	tcc Ser	acc Thr 225	caa Gln	ata Ile	tcc Ser	ttc Phe	gtg Val 230	gca Ala	gga Gly	gag Glu	aag Lys	784
atg Met 235	gat Asp	ctg Leu	aac Asn	acc Thr	agc Ser 240	gac Asp	atc Ile	atg Met	cag Gln	gtg Val 245	tcc Ser	ctg Leu	tat Tyr	ggc Gly	tac Tyr 250	832
gta Val	tac Tyr	acg Thr	ctc Leu	tac Tyr 255	aca Thr	cac His	agc Ser	ttc Phe	cag Gln 260	tgc Cys	tat Tyr	ggc Gly	cgg Arg	aat Asn	gag Glu 265	880
gct Ala	gag Glu	aag Lys	aag Lys 270	ttt Phe	ctg Leu	gca Ala	atg Met	ctc Leu 275	ctg Leu	cag Gln	aat Asn	tct Ser	cct Pro 280	acc Thr	aaa Lys	928
aac Asn	cat His	ctc Leu 285	acc Thr	aat Asn	ccc Pro	tgt Cys	tac Tyr 290	cct Pro	cgg Arg	gat Asp	tat Tyr	agc Ser	atc Ile	agc Ser	ttc Phe	976
acc Thr	atg Met 300	ggc Gly	cat His	gta Val	ttt Phe	gat Asp 305	agc Ser	ctg Leu	tgc Cys	act Thr	gtg Val 310	gac Asp	cag Gln	agg Arg	cca Pro	1024
gaa Glu 315	agt Ser	tat Tyr	aac Asn	ccc Pro	aat Asn 320	gat Asp	gtc Val	atc Ile	act Thr	ttt Phe 325	gaa Glu	gga Gly	act Thr	ggg Gly	gac Asp 330	1072
cca Pro	tct Ser	ctg Leu	tgt Cys	aag Lys 335	gag Glu	aag Lys	gtg Val	gct Ala	tcc Ser	ata Ile	ttt Phe	gac Asp	ttc Phe	aaa Lys	gct Ala 345	1120
tgc Cys	cat His	gat Asp	caa Gln	gaa Glu	acc Thr	tgt Cys	tct Ser	ttt Phe 355	gat Asp	ggg Gly	gtt Val	tat Tyr	cag Gln	cca Pro	aag Lys	1168
att Ile	aaa Lys	ggg Gly 365	cca Pro	ttt Phe	gtg Val	gct Ala	ttt Phe 370	gca Ala	gga Gly	ttc Phe	tac Tyr	tac Tyr	aca Thr	gcc Ala	agt Ser	1216
gct Ala	tta Leu 380	aat Asn	ctt Leu	tca Ser	ggt Gly	agc Ser	ttt Phe 385	tcc Ser	ctg Leu	gac Asp	acc Thr	ttc Phe	aac Asn	tcc Ser	agc Ser	1264

acc tgg aat ttc tgc tca cag aat tgg agt cag ctc cca ctg ctg ctc	1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu	
395 400 405 410	
ccc aaa ttt gat gag gta tat gcc cgc tct tac tgc ttc tca gcc aac	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn	
415 420 425	
tac atc tac cac ttg ttt gtg aac ggt tac aaa ttc aca gag gag act	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr	
430 435 440	
tgg ccc caa ata cac ttt gaa aaa gaa gtg ggg aat agc agc ata gcc	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala	
445 450 455	
tgg tct ctt ggc tac atg ctc agc ctg acc aac cag atc cca gct gaa	1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	
460 465 470	
agc cct ctg atc cgt ctg ccc ata gaa cca cct gtc ttt gtg ggc acc	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	
475 480 485 490	
ctc gct ttc ttc aca gtg gca gcc ttg ctg tgt ctg gca ttt ctt gca	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
tac ctg tgt tca gca acc aga aga aag agg cac tcc gag cat gcc ttt	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
gac cat gca gtg gat tct gac tgagccttca aagcagctcc tggagtccaa	1699
Asp His Ala Val Asp Ser Asp	
525	
tggtctgctta gagtcagcct ggggtggcacc aggcaatgca ggtgaagtgg ctgccttcag	1759
gaaatacaac taactaaaat caaacaccta ggtcacgtgc ctctcaaata ctgatttctg	1819
ccacagcacc tcttgaggca tcccttggct attctgtgca tattgttctt cagagacctc	1879
actaccacaca tgctgatcta ttgggggaaca gagaagagac aggccactaa ggtcaggctc	1939
tttatattaa gttccccaga ggaagagtaa gttgagaagg tatcagttta atgttgaaga	1999
attgacctca gggctcagtt tccatttccc tccctcagta ttcttcttgg caagataccc	2059
attaagcatt tcgccaatca gaatctcatt ttatagtttt tcccattggg ctttaactaa	2119
gactttcttg tagcaatctc gtaagcagtg aacccctca gatcagtaga atatagtatc	2179
tgggggagaa gacttacttc cttcagggca gcagccacag ccaggcttct gtcatacagg	2239
tagatccoga agcacagaga cataaaaaag gtctcccaga aaactataga ccattctcca	2299
agtggaattc ccacttaggg ctctgtgtcac tagattgcaa cctgtgtgtt tgtcatcatc	2359

ctcatctcac cattgtattg ctatgccctc ccataaaaaac acattgatcc ctagcaagat 2419
tattgcattc cagattttac tgcctttgct aggtttttgc ttagcaaagg gctgactttc 2479
cattgttata atggtgtata tattttttgct accattccca caagtatact tgatgttgtc 2539
atagaacgaa catcctactc tatgatttac taaccaatta ctttcccaga tcatagacct 2599
ctctgcatag tagtcatagg tcttgacttt ggggaaagaa aaggaagctg caggaatatt 2659
tatctccaaa gtcgaatgag aaagaactcc agcaaatacca atggctacaa actaaaaatc 2719
agcattatatt catattgctg tttcttagct gaatatggaa taaagaacta ttattttatt 2779
ttgaaaaaaaa aaaaaaaaaa 2797

<210> 4
<211> 529
<212> PRT
<213> Homo sapiens

<400> 4
Met Phe Thr Val Leu Thr Arg Gln Pro Cys Glu Gln Ala Gly Leu Lys
1 5 10 15
Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala Leu Val Val Leu Leu Val
20 25 30
Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
35 40 45
Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
50 55 60
Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
65 70 75 80
Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
85 90 95
Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
100 105 110
Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
115 120 125
His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
130 135 140
Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu Val Leu Glu Ser Ile
145 150 155 160
Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
165 170 175
Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
180 185 190

Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala Tyr Leu Cys Ser Ala Thr
500 505 510

Arg Arg Lys Arg His Ser Glu His Ala Phe Asp His Ala Val Asp Ser
515 520 525

Asp

<210> 5
<211> 1998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (247)..(1530)

<400> 5
gcgcgcgcgt tttccttggt cctgggtcaac aaagaaatgt ggagtgtctt ggctgaatcc 60
tcatacagac aagatcatta tgggtgctgtt aggtaggact tgtatccaga tgtaagggtg 120
aaaaagtgat ataataaagg aaccaaggag aaaattcaga aggaaagaaa aaattgcctc 180
tgcaggtgtg cgagcaggat tgcttctgca acaaaagcct ccaccagacc acatcttggg 240
aaaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10
tcc tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15 20 25 30
gag ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45
acc ttg tat gga att atg ttt gat gca ggg agc act gga act cga att 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60
cat gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta 480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
65 70 75
gaa ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta 528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val
80 85 90
gat caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg 576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val
95 100 105 110

Tyr	Thr	Phe	Val	Gln	Lys	Met	Pro	Gly	Gln	Leu	Pro	Ile	Leu	Glu	Gly	65	70	75	80
Glu	Val	Phe	Asp	Ser	Val	Lys	Pro	Gly	Leu	Ser	Ala	Phe	Val	Asp	Gln	85	90	95	
Pro	Lys	Gln	Gly	Ala	Glu	Thr	Val	Gln	Gly	Leu	Leu	Glu	Val	Ala	Lys	100	105	110	
Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Lys	Lys	Thr	Pro	Val	Val	Leu	Lys	115	120	125	
Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	His	Lys	Ala	Lys	Ala	Leu	130	135	140	
Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu	Val	Pro	145	150	155	160
Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala	165	170	175	
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln	180	185	190	
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	195	200	205	
Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr	210	215	220	
Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	Thr	His	225	230	235	240
Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255	
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys	260	265	270	
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	275	280	285	
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300	
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315	320
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335	
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350	
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365	

[illegible]

```
<220>  
<221> CDS  
<222> (205) .. (1599)
```

15

<213> Mus musculus

<400> 8

Met Ala Thr Ser Trp Gly Ala Val Phe Met Leu Ile Ile Ala Cys Val
1 5 10 15
Gly Ser Thr Val Phe Tyr Arg Glu Gln Gln Thr Trp Phe Glu Gly Val
20 25 30
Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr
35 40 45
Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
50 55 60
Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
65 70 75 80
Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
85 90 95
Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
100 105 110
Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
115 120 125
Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
130 135 140
Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
145 150 155 160
Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
165 170 175
Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
180 185 190
Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
195 200 205
Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
210 215 220
Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
225 230 235 240
Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
245 250 255
Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
260 265 270
Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
 290 295 300
 Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
 305 310 315 320
 Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
 325 330 335
 Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
 340 345 350
 Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
 355 360 365
 Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
 370 375 380
 Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
 385 390 395 400
 His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
 405 410 415
 Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
 420 425 430
 Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val
 435 440 445
 Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr
 450 455 460
 Arg
 465
 <210> 9
 <211> 428
 <212> PRT
 <213> Homo sapiens
 <400> 9
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15
 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30
 Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45
 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60
 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80

Glu	Val	Phe	Asp	Ser	Val	Lys	Pro	Gly	Leu	Ser	Ala	Phe	Val	Asp	Gln	85	90	95
Pro	Lys	Gln	Gly	Ala	Glu	Thr	Val	Gln	Gly	Leu	Leu	Glu	Val	Ala	Lys	100	105	110
Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Lys	Lys	Thr	Pro	Val	Val	Leu	Lys	115	120	125
Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	His	Lys	Ala	Lys	Ala	Leu	130	135	140
Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu	Val	Pro	145	150	155
Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala	165	170	175
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln	180	185	190
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	195	200	205
Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr	210	215	220
Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	Thr	His	225	230	235
Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys	260	265	270
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	275	280	285
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr	370	375	380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 10

<211> 455

<212> PRT

<213> P. sativum

<400> 10

Met Glu Leu Leu Ile Lys Leu Ile Thr Phe Leu Leu Phe Ser Met Pro
1 5 10 15

Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn Leu Leu Thr Ser Arg
20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
210 215 220

Pro	Leu	Arg	Arg	His	Leu	Leu	Ser	His	Glu	Ser	Glu	His	Tyr	Ala	Val	35	40	45	
Ile	Phe	Asp	Ala	Gly	Ser	Thr	Gly	Ser	Arg	Val	His	Val	Phe	Arg	Phe	50	55	60	
Asp	Glu	Lys	Leu	Gly	Leu	Leu	Pro	Ile	Gly	Asn	Asn	Ile	Glu	Tyr	Phe	65	70	75	80
Met	Ala	Thr	Glu	Pro	Gly	Leu	Ser	Ser	Tyr	Ala	Glu	Asp	Pro	Lys	Ala	85	90	95	
Ala	Ala	Asn	Ser	Leu	Glu	Pro	Leu	Leu	Asp	Gly	Ala	Glu	Gly	Val	Val	100	105	110	
Pro	Gln	Glu	Leu	Gln	Ser	Glu	Thr	Pro	Leu	Glu	Leu	Gly	Ala	Thr	Ala	115	120	125	
Gly	Leu	Arg	Met	Leu	Lys	Gly	Asp	Ala	Ala	Glu	Lys	Ile	Leu	Gln	Ala	130	135	140	
Val	Arg	Asn	Leu	Val	Lys	Asn	Gln	Ser	Thr	Phe	His	Ser	Lys	Asp	Gln	145	150	155	160
Trp	Val	Thr	Ile	Leu	Asp	Gly	Thr	Gln	Glu	Gly	Ser	Tyr	Met	Trp	Ala	165	170	175	
Ala	Ile	Asn	Tyr	Leu	Leu	Gly	Asn	Leu	Gly	Lys	Asp	Tyr	Lys	Ser	Thr	180	185	190	
Thr	Ala	Thr	Ile	Asp	Leu	Gly	Gly	Gly	Ser	Val	Gln	Met	Ala	Tyr	Ala	195	200	205	
Ile	Ser	Asn	Glu	Gln	Phe	Ala	Lys	Ala	Pro	Gln	Asn	Glu	Asp	Gly	Glu	210	215	220	
Pro	Tyr	Val	Gln	Gln	Lys	His	Leu	Met	Ser	Lys	Asp	Tyr	Asn	Leu	Tyr	225	230	235	240
Val	His	Ser	Tyr	Leu	Asn	Tyr	Gly	Gln	Leu	Ala	Gly	Arg	Ala	Glu	Ile	245	250	255	
Phe	Lys	Ala	Ser	Arg	Asn	Glu	Ser	Asn	Pro	Cys	Ala	Leu	Glu	Gly	Cys	260	265	270	
Asp	Gly	Tyr	Tyr	Ser	Tyr	Gly	Gly	Val	Asp	Tyr	Lys	Val	Lys	Ala	Pro	275	280	285	
Lys	Lys	Gly	Ser	Ser	Trp	Lys	Arg	Cys	Arg	Arg	Leu	Thr	Arg	His	Ala	290	295	300	
Leu	Lys	Ile	Asn	Ala	Lys	Cys	Asn	Ile	Glu	Glu	Cys	Thr	Phe	Asn	Gly	305	310	315	320
Val	Trp	Asn	Gly	Gly	Gly	Gly	Asp	Gly	Gln	Lys	Asn	Ile	His	Ala	Ser	325	330	335	

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
 340 345 350
 Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
 355 360 365
 Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
 370 375 380
 Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
 385 390 395 400
 Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
 405 410 415
 Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
 420 425 430
 Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
 435 440 445
 Ile Arg Val Ala Ser Ser
 450

<210> 12
 <211> 473
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 12
 Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
 1 5 10 15
 Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
 20 25 30
 Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
 35 40 45
 Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
 50 55 60
 Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
 65 70 75 80
 Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
 85 90 95
 Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
 100 105 110
 Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
 115 120 125
 Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
 130 135 140

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
 450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
 465 470

<210> 13
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 13
 Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
 1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
 20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
 35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
 50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
 65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
 85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
 100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
 115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
 130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
 145 150

<210> 14
 <211> 154
 <212> PRT
 <213> Rattus norvegicus

<400> 14
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
 1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
 35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys
85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
145 150

<210> 15
<211> 153
<212> PRT
<213> Homo sapiens

<400> 15
Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16
 <211> 150
 <212> PRT
 <213> Gallus gallus

<400> 16
 Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val
 1 5 10 15
 Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val
 20 25 30
 Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr
 35 40 45
 Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser
 50 55 60
 Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu
 65 70 75 80
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro
 85 90 95
 Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr
 100 105 110
 Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Glu Gly
 115 120 125
 Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
 130 135 140
 Arg Gly Trp Leu Gly Glu
 145 150

<210> 17
 <211> 148
 <212> PRT
 <213> Caenorhabditis elegans

<400> 17
 Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu
 1 5 10 15
 Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp
 20 25 30
 Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly
 35 40 45
 Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr
 50 55 60
 Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly
 65 70 75 80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
130 135 140

Gly Arg Phe Asp
145

<210> 18
<211> 10
<212> RNA
<213> Mus musculus

<400> 18
aagaauaugg 10

<210> 19
<211> 10
<212> RNA
<213> Vertebrate

<400> 19
gccgccaugg 10

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ccagactgta aatcttttgg 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
aggggaatgta ataagggtag 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 22

ctgcttgagt gacgtctctg

20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

cacatgaggt tcagctcgtg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

gtgaagtggc tgccttcagg

20

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

cctttgactc gggactccag

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 26

gaactgctgc ctaaccactc

20

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
attgatgggt cttgggattg c 21

<210> 28
<211> 10
<212> RNA
<213> Homo sapiens

<400> 28
augugaauga 10

<210> 29
<211> 10
<212> RNA
<213> Homo sapiens

<400> 29
acaaggauga 10



Creation date: 10-14-2003
 Indexing Officer: KNGUYEN6 - KIM NGUYEN
 Team: OIPEBackFileIndexing
 Dossier: 09905732

Legal Date: 01-23-2002

No.	Doccode	Number of pages
1	CRFL	6

Total number of pages: 6

Remarks:

Order of re-scan issued on



A DOCPHOENIX

APPL PARTS

____ IMIS _____
Internal Misc. Paper

____ LET. _____
Misc. Incoming Letter

____ 371P _____
PCT Papers in a 371 Application

____ A... _____
Amendment Including Elections

____ ABST _____
Abstract

____ ADS _____
Application Data Sheet

____ AF/D _____
Affidavit or Exhibit Received

____ APPENDIX _____
Appendix

____ ARTIFACT _____
Artifact

____ BIB _____
Bib Data Sheet

____ CLM _____
Claim

____ COMPUTER _____
Computer Program Listing

____ CRFL _____
All CRF Papers for Backfile

____ DIST _____
Terminal Disclaimer Filed

____ DRW _____
Drawings

____ FOR _____
Foreign Reference

____ FRPR _____
Foreign Priority Papers

____ IDS _____
IDS Including 1449

____ NPL _____
Non-Patent Literature

____ OATH _____
Oath or Declaration

____ PET. _____
Petition

____ RETMAIL _____
Mail Returned by USPS

____ SEQLIST _____
Sequence Listing

____ SPEC _____
Specification

____ SPEC NO _____
Specification Not in English

____ TRNA _____
Transmittal New Application

____ CTNF _____
Count Non-Final

____ CTRS _____
Count Restriction

____ EXIN _____
Examiner Interview

____ M903 _____
DO/EO Acceptance

____ M905 _____
DO/EO Missing Requirement

____ NFDR _____
Formal Drawing Required

____ NOA _____
Notice of Allowance

____ PETDEC _____
Petition Decision

OUTGOING

____ CTMS _____
Misc. Office Action

____ 1449 _____
Signed 1449

____ 892 _____
892

____ ABN _____
Abandonment

____ APDEC _____
Board of Appeals Decision

____ APEA _____
Examiner Answer

____ CTAV _____
Count Advisory Action

____ CTEQ _____
Count Ex parte Quayle

____ CTFR _____
Count Final Rejection

INCOMING

____ AP.B _____
Appeal Brief

____ C.AD _____
Change of Address

____ N/AP _____
Notice of Appeal

____ PA.. _____
Change in Power of Attorney

____ REM _____
Applicant Remarks in Amendment

____ XT/ _____
Extension of Time filed separate

Internal

____ SRNT _____
Examiner Search Notes

____ CLMPTO _____
PTO Prepared Complete Claim Set

____ ECBOX _____
Evidence Copy Box Identification

____ WCLM _____
Claim Worksheet

____ WFEE _____
Fee Worksheet

File Wrapper

____ FWCLM _____
File Wrapper Claim

____ IIFW _____
File Wrapper Issue Information

____ SRFW _____
File Wrapper Search Info